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OIPE

RAW SEQUENCE LISTING

DATE: 05/02/2002

PATENT APPLICATION: US/10/002,309B

TIME: 16:51:05

Input Set : A:\10002309SequenceListing.txt

Output Set: N:\CRF3\05022002\J002309B.raw

3 <110> APPLICANT: WISCONSIN ALUMNI RESEARCH FOUNDATION
 5 <120> TITLE OF INVENTION: E. COLI O157:H7 C1 ESTERASE INHIBITOR-BINDING PROTEIN AND
 METHODS OF USE
 7 <130> FILE REFERENCE: 096429-9117
 9 <140> CURRENT APPLICATION NUMBER: 10/002,309B
 C--> 10 <141> CURRENT FILING DATE: 2002-04-19
 12 <150> PRIOR APPLICATION NUMBER: 60/243,675
 13 <151> PRIOR FILING DATE: 2000-10-26
 15 <160> NUMBER OF SEQ ID NOS: 17
 17 <170> SOFTWARE: PatentIn version 3.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 2798
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Unknown
 24 <220> FEATURE:
 25 <223> OTHER INFORMATION: Description of Unknown Organism: E. coli O157:H7 plasmid
 p0157
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (138)..(2798)
 30 <223> OTHER INFORMATION:
 33 <400> SEQUENCE: 1
 34 tttagcgaac aggtgtaaat atgttataaa aataaccaac gactagttaa taagtgcgtc 60
 36 ctgaaaaaat aaaatataga aatactgtta tatccggctg catgaacact aaaatgaatg 120
 38 agagatggag aacaccg atg aaa tta aag tat ctg tca tgt acg atc ctt 170
 39 Met Lys Leu Lys Tyr Leu Ser Cys Thr Ile Leu
 40 1 5 10
 42 gcc cct ctg gcg att ggg gta ttt tct gca aca gct gct gat aat aat 218
 43 Ala Pro Leu Ala Ile Gly Val Phe Ser Ala Thr Ala Ala Asp Asn Asn
 44 15 20 25
 46 tca gcc att tat ttc aat acc tcc cag cct ata aat gat ctg cag ggt 266
 47 Ser Ala Ile Tyr Phe Asn Thr Ser Gln Pro Ile Asn Asp Leu Gln Gly
 48 30 35 40
 50 tcg ttg gcc gca gag gtg aaa ttt gca caa agc cag att tta ccc gcc 314
 51 Ser Leu Ala Ala Glu Val Lys Phe Ala Gln Ser Gln Ile Leu Pro Ala
 52 45 50 55
 54 cat cct aaa gaa ggg gat agt caa cca cat ctg acc agc ctg cgg aaa 362
 55 His Pro Lys Glu Gly Asp Ser Gln Pro His Leu Thr Ser Leu Arg Lys
 56 60 65 70 75
 58 agt ctg ctg ctt gtc cgt ccg gtg aaa gct gat gat aaa aca cct gtt 410
 59 Ser Leu Leu Leu Val Arg Pro Val Lys Ala Asp Asp Lys Thr Pro Val
 60 80 85 90
 62 cag gtg gaa gcc cgc gat gat aat aat aaa att ctc ggt acg tta acc 458
 63 Gln Val Glu Ala Arg Asp Asp Asn Asn Lys Ile Leu Gly Thr Leu Thr

64

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66	ctt	tat	cct	cct	tca	tca	cta	ccg	gat	aca	atc	tac	cat	ctg	gat	ggt	506
67	Leu	Tyr	Pro	Pro	Ser	Ser	Leu	Pro	Asp	Thr	Ile	Tyr	His	Leu	Asp	Gly	
68			110					115					120				
70	gtt	ccg	gaa	ggt	ggt	atc	gat	ttc	aca	cct	cat	aat	gga	acg	aaa	aag	554
71	Val	Pro	Glu	Gly	Gly	Ile	Asp	Phe	Thr	Pro	His	Asn	Gly	Thr	Lys	Lys	
72		125					130					135					
74	atc	att	aat	acg	gtg	gct	gaa	gta	aac	aaa	ctc	agt	gat	gcc	agc	ggg	602
75	Ile	Ile	Asn	Thr	Val	Ala	Glu	Val	Asn	Lys	Leu	Ser	Asp	Ala	Ser	Gly	
76	140					145					150					155	
78	agt	tct	att	cat	agc	cat	cta	aca	aat	aat	gca	ctg	gtg	gag	atc	cat	650
79	Ser	Ser	Ile	His	Ser	His	Leu	Thr	Asn	Asn	Ala	Leu	Val	Glu	Ile	His	
80				160					165					170			
82	act	gca	aat	ggt	cgt	tgg	gta	aga	gac	att	tat	ctg	ccg	cag	gga	ccc	698
83	Thr	Ala	Asn	Gly	Arg	Trp	Val	Arg	Asp	Ile	Tyr	Leu	Pro	Gln	Gly	Pro	
84			175					180						185			
86	gac	ctt	gaa	ggt	aag	atg	gtt	cgc	ttt	gtt	tcg	tct	gca	ggc	tat	agt	746
87	Asp	Leu	Glu	Gly	Lys	Met	Val	Arg	Phe	Val	Ser	Ser	Ala	Gly	Tyr	Ser	
88		190						195					200				
90	tca	acg	gtt	ttt	tat	ggt	gat	cga	aaa	gtc	aca	ctc	tcg	gtg	ggt	aac	794
91	Ser	Thr	Val	Phe	Tyr	Gly	Asp	Arg	Lys	Val	Thr	Leu	Ser	Val	Gly	Asn	
92		205					210					215					
94	act	ctt	ctg	ttc	aaa	tat	gta	aat	ggt	cag	tgg	ttc	cgc	tcc	ggt	gaa	842
95	Thr	Leu	Leu	Phe	Lys	Tyr	Val	Asn	Gly	Gln	Trp	Phe	Arg	Ser	Gly	Glu	
96	220				225					230					235		
98	ctg	gag	aat	aat	cga	atc	act	tat	gct	cag	cat	att	tgg	agt	gct	gaa	890
99	Leu	Glu	Asn	Asn	Arg	Ile	Thr	Tyr	Ala	Gln	His	Ile	Trp	Ser	Ala	Glu	
100				240					245					250			
102	ctg	cct	gcg	cac	tgg	atc	gtg	cct	ggt	tta	aac	ttg	gtg	att	aaa	cag	938
103	Leu	Pro	Ala	His	Trp	Ile	Val	Pro	Gly	Leu	Asn	Leu	Val	Ile	Lys	Gln	
104			255					260						265			
106	ggc	aat	ctg	agc	ggt	cgc	cta	aat	gat	atc	aag	att	gga	gca	ccg	ggt	986
107	Gly	Asn	Leu	Ser	Gly	Arg	Leu	Asn	Asp	Ile	Lys	Ile	Gly	Ala	Pro	Gly	
108		270					275						280				
110	gag	ctg	ttg	ttg	cat	aca	att	gat	atc	ggg	atg	ttg	acc	act	ccc	cgg	1034
111	Glu	Leu	Leu	Leu	His	Thr	Ile	Asp	Ile	Gly	Met	Leu	Thr	Thr	Pro	Arg	
112		285					290					295					
114	gat	cgc	ttt	gat	ttt	gcc	aaa	gac	aaa	gaa	gca	cat	agg	gaa	tat	ttc	1082
115	Asp	Arg	Phe	Asp	Phe	Ala	Lys	Asp	Lys	Glu	Ala	His	Arg	Glu	Tyr	Phe	
116	300				305					310					315		
118	cag	acc	att	cct	gta	agt	cgt	atg	att	gtt	aat	aat	tat	gcg	cct	cta	1130
119	Gln	Thr	Ile	Pro	Val	Ser	Arg	Met	Ile	Val	Asn	Asn	Tyr	Ala	Pro	Leu	
120				320						325				330			
122	cac	cta	aag	gaa	gtt	atg	tta	cca	acc	gga	gag	tta	ttg	aca	gat	atg	1178
123	His	Leu	Lys	Glu	Val	Met	Leu	Pro	Thr	Gly	Glu	Leu	Leu	Thr	Asp	Met	
124			335					340						345			
126	gat	cca	gga	aat	ggt	ggg	tgg	cat	agt	ggt	aca	atg	cgt	caa	aga	ata	1226
127	Asp	Pro	Gly	Asn	Gly	Gly	Trp	His	Ser	Gly	Thr	Met	Arg	Gln	Arg	Ile	
128			350					355					360				
130	ggt	aaa	gaa	ttg	gtt	tcg	cat	ggc	att	gat	aat	gct	aac	tat	ggt	tta	1274

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131	Gly	Lys	Glu	Leu	Val	Ser	His	Gly	Ile	Asp	Asn	Ala	Asn	Tyr	Gly	Leu	
132		365					370				375						
134	aat	agt	acc	gca	ggc	tta	ggg	gag	aat	agt	cat	cca	tat	gta	gtt	gcg	1322
135	Asn	Ser	Thr	Ala	Gly	Leu	Gly	Glu	Asn	Ser	His	Pro	Tyr	Val	Val	Ala	
136	380					385					390					395	
138	caa	tta	gcg	gca	cat	aat	agc	cgc	ggt	aat	tat	gct	aat	ggc	atc	cag	1370
139	Gln	Leu	Ala	Ala	His	Asn	Ser	Arg	Gly	Asn	Tyr	Ala	Asn	Gly	Ile	Gln	
140					400				405					410			
142	gtt	cat	ggt	ggc	tcc	gga	ggt	ggg	gga	att	gtt	act	tta	gat	tcc	aca	1418
143	Val	His	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ile	Val	Thr	Leu	Asp	Ser	Thr	
144			415				420				425						
146	ttg	ggg	aat	gag	ttc	agt	cat	gaa	gtt	ggt	cat	aat	tat	ggt	ctt	ggt	1466
147	Leu	Gly	Asn	Glu	Phe	Ser	His	Glu	Val	Gly	His	Asn	Tyr	Gly	Leu	Gly	
148		430					435				440						
150	cat	tat	gta	gat	ggt	ttc	aag	ggt	tct	gta	cat	cgt	agt	gca	gaa	aat	1514
151	His	Tyr	Val	Asp	Gly	Phe	Lys	Gly	Ser	Val	His	Arg	Ser	Ala	Glu	Asn	
152		445				450					455						
154	aac	aac	tca	act	tgg	gga	tgg	gat	ggt	gat	aaa	aaa	cgg	ttt	att	cct	1562
155	Asn	Asn	Ser	Thr	Trp	Gly	Trp	Asp	Gly	Asp	Lys	Lys	Arg	Phe	Ile	Pro	
156	460				465				470						475		
158	aac	ttt	tat	ccg	tct	caa	aca	aat	gaa	aag	agt	tgt	ctg	aat	aat	cag	1610
159	Asn	Phe	Tyr	Pro	Ser	Gln	Thr	Asn	Glu	Lys	Ser	Cys	Leu	Asn	Asn	Gln	
160			480				485				490						
162	tgt	caa	gaa	ccg	ttt	gat	gga	cac	aaa	ttt	ggt	ttt	gac	gcc	atg	gcg	1658
163	Cys	Gln	Glu	Pro	Phe	Asp	Gly	His	Lys	Phe	Gly	Phe	Asp	Ala	Met	Ala	
164			495				500				505						
166	gga	ggc	agc	cct	ttc	tct	gct	gca	aac	cgt	ttc	aca	atg	tat	act	ccg	1706
167	Gly	Gly	Ser	Pro	Phe	Ser	Ala	Ala	Asn	Arg	Phe	Thr	Met	Tyr	Thr	Pro	
168		510				515					520						
170	aat	tca	tcg	gct	atc	atc	cag	cgt	ttt	ttt	gaa	aat	aaa	gct	gtg	ttc	1754
171	Asn	Ser	Ser	Ala	Ile	Ile	Gln	Arg	Phe	Phe	Glu	Asn	Lys	Ala	Val	Phe	
172		525				530					535						
174	gat	agc	cgt	tcc	tcc	acc	ggc	ttc	agc	aag	tgg	aat	gca	gat	acg	cag	1802
175	Asp	Ser	Arg	Ser	Ser	Thr	Gly	Phe	Ser	Lys	Trp	Asn	Ala	Asp	Thr	Gln	
176	540				545				550						555		
178	gaa	atg	gaa	ccg	tat	gaa	cac	acc	att	gac	cgt	gcg	gag	cag	att	acg	1850
179	Glu	Met	Glu	Pro	Tyr	Glu	His	Thr	Ile	Asp	Arg	Ala	Glu	Gln	Ile	Thr	
180			560				565							570			
182	gct	tca	gtc	aat	gag	cta	agt	gaa	agc	aaa	atg	gct	gag	ctg	atg	gca	1898
183	Ala	Ser	Val	Asn	Glu	Leu	Ser	Glu	Ser	Lys	Met	Ala	Glu	Leu	Met	Ala	
184			575				580				585						
186	gag	tac	gct	gtc	gtc	aaa	gtg	cat	atg	tgg	aac	ggt	aac	tgg	aca	aga	1946
187	Glu	Tyr	Ala	Val	Val	Lys	Val	His	Met	Trp	Asn	Gly	Asn	Trp	Thr	Arg	
188		590				595					600						
190	aac	atc	tat	atc	cct	aca	gcc	tcc	gca	gat	aat	aga	ggc	agt	atc	ctg	1994
191	Asn	Ile	Tyr	Ile	Pro	Thr	Ala	Ser	Ala	Asp	Asn	Arg	Gly	Ser	Ile	Leu	
192		605				610					615						
194	acc	atc	aac	cat	gag	gcc	ggt	tat	aat	agt	tat	ctg	ttt	ata	aat	ggt	2042
195	Thr	Ile	Asn	His	Glu	Ala	Gly	Tyr	Asn	Ser	Tyr	Leu	Phe	Ile	Asn	Gly	

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196	620	625	630	635	
198	gac gaa aag gtc gtt tcc cag ggg tat aaa aag agc ttt gtt tcc gat	2090			
199	Asp Glu Lys Val Val Ser Gln Gly Tyr Lys Lys Ser Phe Val Ser Asp				
200	640 645 650				
202	ggt cag ttc tgg aaa gaa cgt gat gtg gtt gat act cgt gaa gcg cgt	2138			
203	Gly Gln Phe Trp Lys Glu Arg Asp Val Val Asp Thr Arg Glu Ala Arg				
204	655 660 665				
206	aag cca gag cag ttt ggt gtt cct gtg acg acc ctg gtg ggg tat tac	2186			
207	Lys Pro Glu Gln Phe Gly Val Pro Val Thr Thr Leu Val Gly Tyr Tyr				
208	670 675 680				
210	gat ccg gaa ggc acg ctg tca agc tac atc tat cct gcg atg tat ggt	2234			
211	Asp Pro Glu Gly Thr Leu Ser Ser Tyr Ile Tyr Pro Ala Met Tyr Gly				
212	685 690 695				
214	gcc tat ggc ttc act tat tcc gat gat agt cag aat cta tcc gat aac	2282			
215	Ala Tyr Gly Phe Thr Tyr Ser Asp Asp Ser Gln Asn Leu Ser Asp Asn				
216	700 705 710 715				
218	gac tgc cag ctg cag gtg gat acg aaa gaa ggg cag ttg cga ttc aga	2330			
219	Asp Cys Gln Leu Gln Val Asp Thr Lys Glu Gly Gln Leu Arg Phe Arg				
220	720 725 730				
222	ctg gct aat cac cgg gct aac aac act gta atg aat aag ttc cat att	2378			
223	Leu Ala Asn His Arg Ala Asn Asn Thr Val Met Asn Lys Phe His Ile				
224	735 740 745				
226	aac gtg cca aca gaa agt cag ccc aca cag gcc aca ttg gtt tgc aat	2426			
227	Asn Val Pro Thr Glu Ser Gln Pro Thr Gln Ala Thr Leu Val Cys Asn				
228	750 755 760				
230	aac aag ata ctg gat acc aaa tcg ctc aca cct gcg cca gaa gga ctt	2474			
231	Asn Lys Ile Leu Asp Thr Lys Ser Leu Thr Pro Ala Pro Glu Gly Leu				
232	765 770 775				
234	acc tat act gta aat ggg cag gca ctt cca gca aaa gaa aac gag gga	2522			
235	Thr Tyr Thr Val Asn Gly Gln Ala Leu Pro Ala Lys Glu Asn Glu Gly				
236	780 785 790 795				
238	tgc atc gtg tcc gtg aat tca ggt aaa cgt tac tgt ttg ccg gtt ggt	2570			
239	Cys Ile Val Ser Val Asn Ser Gly Lys Arg Tyr Cys Leu Pro Val Gly				
240	800 805 810				
242	caa cgg tca gga tat agc ctt cct gac tgg att gtt ggg cag gaa gtc	2618			
243	Gln Arg Ser Gly Tyr Ser Leu Pro Asp Trp Ile Val Gly Gln Glu Val				
244	815 820 825				
246	tat gtc gac agc ggg gct aaa gcg aaa gtg ctg ctt tct gac tgg gat	2666			
247	Tyr Val Asp Ser Gly Ala Lys Ala Lys Val Leu Leu Ser Asp Trp Asp				
248	830 835 840				
250	aac ctg tcc tat aac agg att ggt gag ttt gta ggt aat gtg aac cca	2714			
251	Asn Leu Ser Tyr Asn Arg Ile Gly Glu Phe Val Gly Asn Val Asn Pro				
252	845 850 855				
254	gct gat atg aaa aaa gtt aaa gcc tgg aac gga cag tat ttg gac ttc	2762			
255	Ala Asp Met Lys Lys Val Lys Ala Trp Asn Gly Gln Tyr Leu Asp Phe				
256	860 865 870 875				
258	agt aaa cct agg tca atg agg gtt gta tat aaa taa	2798			
259	Ser Lys Pro Arg Ser Met Arg Val Val Tyr Lys				
260	880 885				

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263 <210> SEQ ID NO: 2
 264 <211> LENGTH: 886
 265 <212> TYPE: PRT
 266 <213> ORGANISM: Unknown
 268 <220> FEATURE:
 269 <223> OTHER INFORMATION: Description of Unknown Organism: E. coli O157:H7 plasmid

p0157

271 <400> SEQUENCE: 2

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274	1				5					10					15	
277	Gly	Val	Phe	Ser	Ala	Thr	Ala	Ala	Asp	Asn	Asn	Ser	Ala	Ile	Tyr	Phe
278				20					25					30		
281	Asn	Thr	Ser	Gln	Pro	Ile	Asn	Asp	Leu	Gln	Gly	Ser	Leu	Ala	Ala	Glu
282				35				40					45			
285	Val	Lys	Phe	Ala	Gln	Ser	Gln	Ile	Leu	Pro	Ala	His	Pro	Lys	Glu	Gly
286		50					55				60					
289	Asp	Ser	Gln	Pro	His	Leu	Thr	Ser	Leu	Arg	Lys	Ser	Leu	Leu	Leu	Val
290	65					70				75					80	
293	Arg	Pro	Val	Lys	Ala	Asp	Asp	Lys	Thr	Pro	Val	Gln	Val	Glu	Ala	Arg
294				85					90					95		
297	Asp	Asp	Asn	Asn	Lys	Ile	Leu	Gly	Thr	Leu	Thr	Leu	Tyr	Pro	Pro	Ser
298				100					105					110		
301	Ser	Leu	Pro	Asp	Thr	Ile	Tyr	His	Leu	Asp	Gly	Val	Pro	Glu	Gly	Gly
302			115					120					125			
305	Ile	Asp	Phe	Thr	Pro	His	Asn	Gly	Thr	Lys	Lys	Ile	Ile	Asn	Thr	Val
306		130					135					140				
309	Ala	Glu	Val	Asn	Lys	Leu	Ser	Asp	Ala	Ser	Gly	Ser	Ser	Ile	His	Ser
310	145					150					155				160	
313	His	Leu	Thr	Asn	Asn	Ala	Leu	Val	Glu	Ile	His	Thr	Ala	Asn	Gly	Arg
314				165						170					175	
317	Trp	Val	Arg	Asp	Ile	Tyr	Leu	Pro	Gln	Gly	Pro	Asp	Leu	Glu	Gly	Lys
318				180					185					190		
321	Met	Val	Arg	Phe	Val	Ser	Ser	Ala	Gly	Tyr	Ser	Ser	Thr	Val	Phe	Tyr
322			195					200					205			
325	Gly	Asp	Arg	Lys	Val	Thr	Leu	Ser	Val	Gly	Asn	Thr	Leu	Leu	Phe	Lys
326		210					215					220				
329	Tyr	Val	Asn	Gly	Gln	Trp	Phe	Arg	Ser	Gly	Glu	Leu	Glu	Asn	Asn	Arg
330	225				230					235					240	
333	Ile	Thr	Tyr	Ala	Gln	His	Ile	Trp	Ser	Ala	Glu	Leu	Pro	Ala	His	Trp
334				245						250					255	
337	Ile	Val	Pro	Gly	Leu	Asn	Leu	Val	Ile	Lys	Gln	Gly	Asn	Leu	Ser	Gly
338				260					265					270		
341	Arg	Leu	Asn	Asp	Ile	Lys	Ile	Gly	Ala	Pro	Gly	Glu	Leu	Leu	Leu	His
342			275					280					285			
345	Thr	Ile	Asp	Ile	Gly	Met	Leu	Thr	Thr	Pro	Arg	Asp	Arg	Phe	Asp	Phe
346		290					295					300				
349	Ala	Lys	Asp	Lys	Glu	Ala	His	Arg	Glu	Tyr	Phe	Gln	Thr	Ile	Pro	Val
350	305					310					315				320	
353	Ser	Arg	Met	Ile	Val	Asn	Asn	Tyr	Ala	Pro	Leu	His	Leu	Lys	Glu	Val
354					325					330					335	

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/002,309B

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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

VERIFICATION SUMMARY

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date